Amendments to the Specification:

Please replace the paragraph beginning at line 17 of page 14 with the following paragraph:

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site ~~http://~~www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

Please replace the paragraph beginning at line 22 of page 15 with the following paragraph:

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al., Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al., J. Mol. Biol.* 215:403-410 (1990). BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (~~http://~~www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either

sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Please replace the paragraph beginning at line 24 of page 20 with the following paragraph:

A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include adriamycin, doxorubicin, epirubicin, 5-fluorouracil, cytosine arabinoside ("Ara-C"), cyclophosphamide, thiotepa, busulfan, cytoxin, taxoids, e.g., paclitaxel (~~Taxol,~~ TAXOL®, Bristol-Myers Squibb Oncology, Princeton, N.J.), and doxetaxel (~~Taxotere,~~TAXOTERE®, ~~Rhne~~ Rhone-Poulenc Rorer, Antony, Rnace), toxotere, methotrexate, cisplatin, melphalan, vinblastine, bleomycin, etoposide, ifosfamide, mitomycin C, mitoxantrone, vincristine, vinorelbine, carboplatin, teniposide, daunomycin, carminomycin, aminopterin, dactinomycin, mitomycins, esperamicins (see U.S. Pat. No. 4,675,187), 5-FU, 6-thioguanine, 6-mercaptopurine, actinomycin D, VP-16, chlorambucil, melphalan, and other related nitrogen mustards. Also included in this definition are hormonal agents that act to regulate or inhibit hormone action on tumors such as tamoxifen and onapristone. such as tamoxifen and onapristone.

Please replace the paragraph beginning at line 1 of page 42 with the following paragraph:

Preparation of total RNA from fresh-frozen prostate and xenograft tissue was performed by extraction with ~~Trizol~~TRIZOL® reagent (Life Technologies, Inc., Gaithersburg, MD) and was reverse transcribed using a primer containing oligodeoxythymidylic acid and a T7 promoter sequence. The resulting cDNAs were then in vitro transcribed in the presence of biotinylated nucleotides (Bio-11-CTP and Bio-16-UTP) using the T7 ~~MEGAscript~~ MEGASCRIPT® kit (Ambion, Austin, TX).

Please replace the paragraph beginning at line 7 of page 42 with the following paragraph:

The biotinylated targets were hybridized to the Eos Hu03, a customized Affymetrix ~~GeneChip~~ GENECHIP® (Affymetrix, Santa Clara, CA) oligonucleotide array comprising 59,619 probesets representing 46,000 unique sequences including both known and FGENESH predicted exons that were based on the first draft of the human genome. The Hu03 probesets consist of perfect match probes only, most probesets having 6 or 7 probes. Hybridization signals were visualized using phycoerythrin-conjugated streptavidin (Molecular Probes, Eugene, OR).

Please replace the paragraph beginning at line 3 of page 48 with the following paragraph:

In order to assay internalization of GPR64 antibodies, cells were placed in an incubator at 37°C for 1 h and then placed on ice for 1 h in blocking solution (20 ug/ml pure Goat anti-mouse antibody in media). After washing in PBS, cells were fixed in 5%

ultra pure formaldehyde. Cells were then washed with 0.5% Triton X-1000 and incubated with ~~AlexaFluor~~ ALEXAFLUOR®-488 goat anti-mouse secondary antibody (1:2200 dilution in chilled growth media; Molecular Probes). Visualization of the internalized antibodies was performed as described above.

Please replace the paragraph beginning at line 9 of page 49 with the following paragraph:

Tissue microarrays of normal tissues and ovarian cancer samples were obtained from Clinomics Biosciences, Inc. (Pittsfield, MA). IHC on formalin-fixed paraffin embedded tissues was carried out using standard methods as previously described (Henshall et al., 2003, Oncogene 22:6005-6012). Heat induced antigen retrieval was performed in Dako Target Retrieval Solution for 15 minutes in a pressure cooker. Samples were then incubated with a GPR64 specific antibody (e.g. GPR64-101) or control mouse IgG1 [TIB191, a mouse anti-trinitrophenol mAb (hybridoma clone 1B76.11, ATCC)] for 30 minutes. Antibody binding was detected using biotinylated secondary antibody [Goat-anti-mouse IgG (3 mg/ml, 30 minutes; Jackson ImmunoResearch)], and developed using the ~~Vectastain~~ VECTASTAIN® Elite ABC Kit (Vector Laboratories) and stable DAB (diaminobenzidine and H2O2; Research Genetics). Staining was performed using the DAKO Autostainer at room temperature.

Please replace the paragraph beginning at line 7 of page 52 with the following paragraph:

This deposit was made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposit will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Protein Design Labs, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon ~~influence~~ issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trade to be entitled thereto according to 35 U.S.C. § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638). All restrictions upon public access to the deposit will be irrevocably removed upon the grant of a patent on this application.